

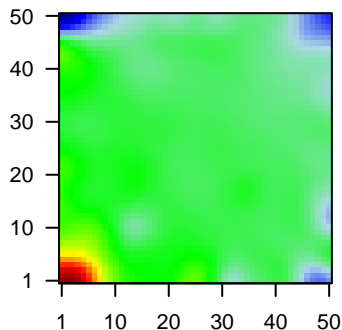
# GW\_064

## Global Summary

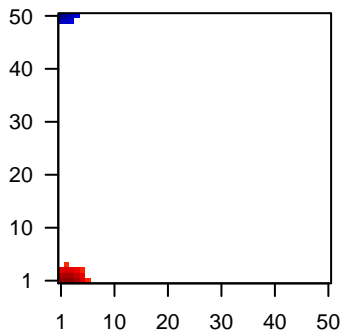
%DE = 0.15  
 # genes with fdr < 0.2 = 2091 ( 1171 + / 920 - )  
 # genes with fdr < 0.1 = 1668 ( 942 + / 726 - )  
 # genes with fdr < 0.05 = 1371 ( 785 + / 586 - )  
 # genes with fdr < 0.01 = 980 ( 568 + / 412 - )  
 # genes in genesets = 16332

<FC> = 0  
 <shrinkage-t> = 0  
 <p-value> = 0.09  
 <fdr> = 0.85

Profile



Regulated Spots



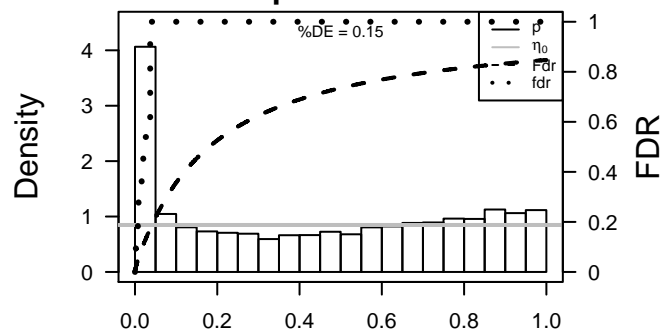
## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	59	1.95	2e-16	3e-14	3 x 1 actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;]
2	72	1.85	2e-16	3e-14	4 x 1 actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
3	131	-2.84	2e-16	3e-14	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	165	1.61	2e-16	3e-14	3 x 1 AE binding protein 1 [Source:HGNC Symbol;Acc:303]
5	113146	1.55	2e-16	3e-14	1 x 44 AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:20125]
6	8644	-2.48	2e-16	3e-14	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sy
7	218	-3.09	2e-16	3e-14	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
8	115701	1.61	2e-16	3e-14	50 x 3 alpha-kinase 2 [Source:HGNC Symbol;Acc:20565]
9	347	1.83	2e-16	3e-14	50 x 7 apolipoprotein D [Source:HGNC Symbol;Acc:612]
10	84707	-1.49	2e-16	3e-14	50 x 48 brain expressed X-linked 2 [Source:HGNC Symbol;Acc:3093
11	633	2.12	2e-16	3e-14	3 x 1 biglycan [Source:HGNC Symbol;Acc:1044]
12	23246	1.68	2e-16	3e-14	1 x 16 block of proliferation 1 [Source:HGNC Symbol;Acc:15519]
13	375791	-1.74	2e-16	3e-14	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Syml
14	760	2.81	2e-16	3e-14	1 x 44 carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
15	51806	-1.69	2e-16	3e-14	4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180]
16	857	1.66	2e-16	3e-14	1 x 4 caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;#
17	1048	-1.66	2e-16	3e-14	2 x 50 carcinoembryonic antigen-related cell adhesion molecule 5 [
18	4680	-1.92	2e-16	3e-14	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
19	91612	2	2e-16	3e-14	24 x 48 churchill domain containing 1 [Source:HGNC Symbol;Acc:20
20	22802	-1.94	2e-16	3e-14	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	19.82	NULL	190	CC extracellular matrix
2	19.77	NULL	250	Lymphoma ENZ_Stromal signature 1
3	17.22	NULL	242	BP extracellular matrix organization
4	15.63	NULL	69	BP extracellular matrix disassembly
5	13.95	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
6	13.59	NULL	64	BP collagen catabolic process
7	12.88	NULL	4	MMML C6S CIEJ_MMML 23
8	12.36	NULL	16	MMML C6S CIEJ_MMML 1
9	12.2	NULL	183	CC proteinaceous extracellular matrix
10	12.05	NULL	11	MF platelet-derived growth factor binding
11	11.88	NULL	534	Chr Chr 8
12	11.13	NULL	83	CC basement membrane
13	10.77	NULL	37	BP collagen fibril organization
14	10.36	NULL	57	MF extracellular matrix structural constituent
15	9.35	NULL	12	miRNA target-29c
16	9.16	NULL	403	BP cell adhesion
17	9.1	NULL	699	Chr Chr 5
18	9.07	NULL	12	BP hemidesmosome assembly
19	8.98	NULL	35	Glo Colman_survival_associated
20	8.97	NULL	68	CC collagen
<i>Underexpressed</i>				
1	-16.05	NULL	572	Disease GUDJ_poriasis up
2	-14.2	NULL	135	H.Tiss WIRTH_Mucosa
3	-12.18	NULL	42	BP keratinization
4	-9.98	NULL	21	CC cornified envelope
5	-9.44	NULL	53	BP keratinocyte differentiation
6	-9.18	NULL	417	H.Tiss WIRTH_Immune system
7	-8.21	NULL	602	Chr Chr 10
8	-7.43	NULL	449	Chr Chr 20
9	-7.14	NULL	51	BP type I interferon signaling pathway
10	-7.07	NULL	16	GSEA C2WANG_BARRETTES_ESOPHAGUS_DN
11	-6.88	NULL	16	GSEA C2CROMER_TUMORIGENESIS_DN
12	-6.68	NULL	8	GSEA C2LIU_CDX2_TARGETS_DN
13	-6.64	NULL	1720	Chr Chr 1
14	-6.5	NULL	274	Lymphoma SPANG_IL21 DN
15	-6.48	NULL	6	GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
16	-6.34	NULL	714	Chr Chr 6
17	-6.12	NULL	19	BP peptide cross-linking
18	-5.92	NULL	312	BP immune response
19	-5.84	NULL	204	BP cytokine-mediated signaling pathway
20	-5.59	NULL	16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_1

p-values



# GW\_064

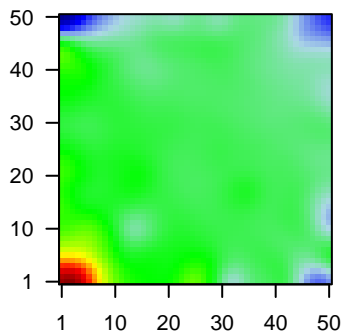
## Local Summary

%DE = 0.9  
 # metagenes = 17  
 # genes = 268  
 # genes in genesets = 267  
 # genes with  $fdr < 0.1$  = 213 ( 206 + / 7 - )  
 # genes with  $fdr < 0.05$  = 201 ( 195 + / 6 - )  
 # genes with  $fdr < 0.01$  = 189 ( 187 + / 2 - )

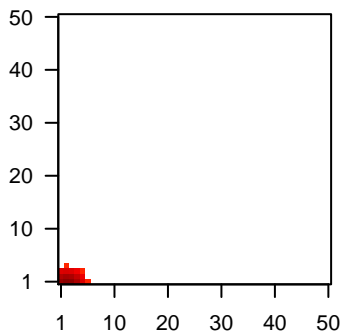
<r> metagenes = 0.96  
 <r> genes = 0.41

<FC> = 0.82  
 <shrinkage-t> = 28.71  
 <p-value> = 0  
 <fdr> = 0.26

Profile



Spot



## Local Genelist

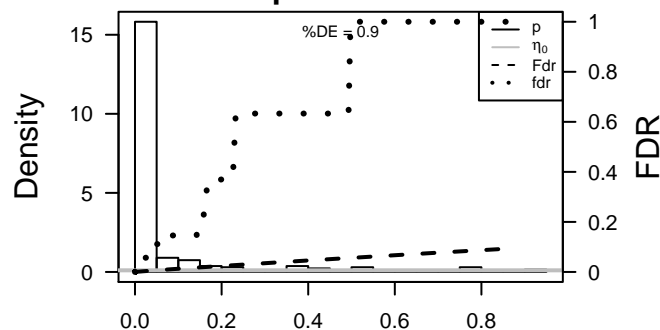
Rank	ID	log(FC)	fdr	p-value	Description
1	59	1.95	2e-16	2e-16	3 x 1 actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;]
2	72	1.85	2e-16	2e-16	4 x 1 actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
3	165	1.61	2e-16	2e-16	3 x 1 AE binding protein 1 [Source:HGNC Symbol;Acc:303]
4	633	2.12	2e-16	2e-16	3 x 1 biglycan [Source:HGNC Symbol;Acc:1044]
5	1277	2.43	2e-16	2e-16	2 x 1 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
6	1278	2.18	2e-16	2e-16	2 x 1 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
7	1281	1.98	2e-16	2e-16	2 x 1 collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
8	1289	1.73	2e-16	2e-16	2 x 1 collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
9	1290	1.99	2e-16	2e-16	2 x 1 collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
10	1291	2.32	2e-16	2e-16	2 x 1 collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211]
11	1293	2.13	2e-16	2e-16	2 x 1 collagen, type VI, alpha 3 [Source:HGNC Symbol;Acc:2213]
12	1464	1.53	2e-16	2e-16	1 x 3 chondroitin sulfate proteoglycan 4 [Source:HGNC Symbol;Acc
13	6374	1.58	2e-16	2e-16	1 x 1 chemokine (C-X-C motif) ligand 5 [Source:HGNC Symbol;Acc
14	3039	2.89	2e-16	2e-16	5 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
15	3040	3.64	2e-16	2e-16	4 x 1 hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
16	3043	3.2	2e-16	2e-16	5 x 1 hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
17	11009	1.74	2e-16	2e-16	1 x 3 interleukin 24 [Source:HGNC Symbol;Acc:11346]
18	3671	1.79	2e-16	2e-16	4 x 1 immunoglobulin superfamily containing leucine-rich repeat [S
19	3956	1.79	2e-16	2e-16	1 x 1 lectin, galactoside-binding, soluble, 1 [Source:HGNC Symbol
20	4312	2.48	2e-16	2e-16	1 x 1 matrix metalloproteinase 1 (interstitial collagenase) [Source:Hi

## Local Geneset Analysis

Overexpression

Rank	GSZ	p-value	#in/all	Geneset
1	43.18	NULL	67 / 190	CC extracellular matrix
2	38.6	NULL	77 / 250	Lymphocyte ENZ_Stromal signature 1
3	37.61	NULL	31 / 69	BP extracellular matrix disassembly
4	36.35	NULL	14 / 16	MMML C6SCIEJ_MMML 1
5	36.26	NULL	12 / 16	GSEA C2FARMER_BREAST_CANCER_CLUSTER_5
6	35.78	NULL	27 / 64	BP collagen catabolic process
7	35.08	NULL	61 / 242	BP extracellular matrix organization
8	34.12	NULL	8 / 11	MF platelet-derived growth factor binding
9	28.16	NULL	2 / 4	MMML C6SCIEJ_MMML 23
10	27.42	NULL	14 / 37	BP collagen fibril organization
11	27.03	NULL	8 / 12	miRNA target-29c
12	25.53	NULL	19 / 57	MF extracellular matrix structural constituent
13	24.98	NULL	37 / 183	CC proteinaceous extracellular matrix
14	24.3	NULL	7 / 15	GSEA C2MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
15	22.66	NULL	11 / 19	MF extracellular matrix binding
16	22.64	NULL	7 / 16	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL
17	22.53	NULL	6 / 13	GSEA C2TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
18	22.48	NULL	10 / 15	GSEA C2ONDER_CDH1_TARGETS_2_UP
19	21.59	NULL	11 / 15	GSEA C2CROMER_TUMORIGENESIS_UP
20	20.33	NULL	4 / 10	BP protein heterotrimerization
21	20.33	NULL	10 / 40	BP cellular response to amino acid stimulus
22	20.14	NULL	5 / 13	GSEA C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
23	19.83	NULL	107 / 1182	CC extracellular region
24	19.56	NULL	81 / 683	CC extracellular space
25	19.51	NULL	12 / 35	Glio Colman_survival_associated
26	19.34	NULL	16 / 68	CC collagen
27	18.45	NULL	7 / 16	GSEA C2ROZANOV_MMP14_TARGETS_SUBSET
28	18.14	NULL	72 / 553	Cancer Lembecke_Colonc Inflammation
29	18.02	NULL	4 / 12	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C2
30	17.34	NULL	5 / 15	GSEA C2TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_N
31	17.2	NULL	5 / 10	GSEA C2KEGG_ECM_RECEPTOR_INTERACTION
32	17.05	NULL	7 / 16	GSEA C2CROONQUIST_STROMAL_STIMULATION_UP
33	17.03	NULL	3 / 14	CC endocytic vesicle lumen
34	16.98	NULL	4 / 8	GSEA C2HAEGERSTRAND_RESPONSE_TO_IMATINIB
35	16.95	NULL	4 / 11	BP dermatan sulfate biosynthetic process
36	16.91	NULL	6 / 10	GSEA C2VERRECCHIA_RESPONSE_TO_TGFB1_C4
37	16.51	NULL	2 / 10	CC hemoglobin complex
38	16.44	NULL	41 / 265	Glio wilscher_GBM_Verhaak-CL_expression_B_up
39	16.44	NULL	41 / 265	Glio wilscher_GBM_Verhaak-MES_expression_B_up
40	16.44	NULL	41 / 265	Glio wilscher_GBM_Verhaak-PNwt_expression_B_down

p-values



# GW\_064

## Local Summary

%DE = 0.94  
 # metagenes = 7  
 # genes = 135  
 # genes in genesets = 132  
 # genes with  $fdr < 0.1$  = 116 ( 11 + / 105 - )  
 # genes with  $fdr < 0.05$  = 115 ( 10 + / 105 - )  
 # genes with  $fdr < 0.01$  = 114 ( 9 + / 105 - )

$\langle r \rangle$  metagenes = 0.99

$\langle r \rangle$  genes = 0.51

$\langle FC \rangle = -0.95$

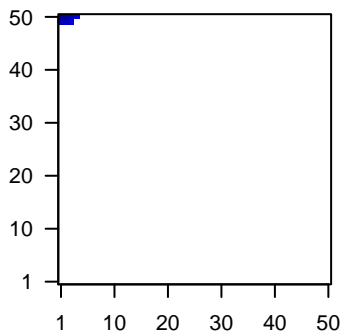
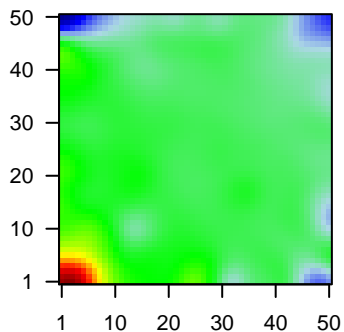
$\langle \text{shrinkage-t} \rangle = -33.53$

$\langle p\text{-value} \rangle = 0$

$\langle fdr \rangle = 0.16$

Profile

Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	131	-2.84	2e-16	5e-17	1 x 50 alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
2	8644	-2.48	2e-16	5e-17	1 x 50 aldo-keto reductase family 1, member C3 [Source:HGNC Sy]
3	218	-3.09	2e-16	5e-17	1 x 50 aldehyde dehydrogenase 3 family, member A1 [Source:HGNC]
4	375791	-1.74	2e-16	5e-17	1 x 50 chromosome 9 open reading frame 169 [Source:HGNC Symt
5	51806	-1.69	2e-16	5e-17	4 x 50 calmodulin-like 5 [Source:HGNC Symbol;Acc:18180]
6	1048	-1.66	2e-16	5e-17	2 x 50 carcinoembryonic antigen-related cell adhesion molecule 5 [
7	4680	-1.92	2e-16	5e-17	1 x 50 carcinoembryonic antigen-related cell adhesion molecule 6 (i
8	22802	-1.94	2e-16	5e-17	1 x 50 chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
9	84518	-1.97	2e-16	5e-17	1 x 50 cornifelin [Source:HGNC Symbol;Acc:30183]
10	54544	-1.54	2e-16	5e-17	1 x 50 cysteine-rich C-terminal 1 [Source:HGNC Symbol;Acc:2987]
11	49860	-2.34	2e-16	5e-17	1 x 50 cornulin [Source:HGNC Symbol;Acc:1230]
12	1673	-1.55	2e-16	5e-17	1 x 49 defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
13	163351	-1.88	2e-16	5e-17	1 x 50 guanylate binding protein family, member 6 [Source:HGNC S]
14	2877	-1.63	2e-16	5e-17	1 x 50 glutathione peroxidase 2 (gastrointestinal) [Source:HGNC Sy]
15	26085	-2.17	2e-16	5e-17	1 x 50 kallikrein-related peptidase 13 [Source:HGNC Symbol;Acc:6]
16	5653	-1.84	2e-16	5e-17	1 x 50 kallikrein-related peptidase 6 [Source:HGNC Symbol;Acc:63]
17	5650	-2.07	2e-16	5e-17	1 x 49 kallikrein-related peptidase 7 [Source:HGNC Symbol;Acc:63]
18	3860	-3.83	2e-16	5e-17	1 x 50 keratin 13 [Source:HGNC Symbol;Acc:6415]
19	3851	-2.47	2e-16	5e-17	1 x 50 keratin 4 [Source:HGNC Symbol;Acc:6441]
20	196374	-1.5	2e-16	5e-17	1 x 50 keratin 78 [Source:HGNC Symbol;Acc:28926]

## Local Geneset Analysis

Underexpression

Rank	GSZ	p-value	#in/all	Geneset
1	-48.69	NULL	57 / 135	H.Tiss WIRTH_Mucosa
2	-26.91	NULL	13 / 42	BP keratinization
3	-24.11	NULL	16 / 53	BP keratinocyte differentiation
4	-22.93	NULL	12 / 21	CC cornified envelope
5	-20.97	NULL	6 / 16	GSEA C2CROMER_TUMORIGENESIS_DN
6	-20.18	NULL	4 / 16	GSEA C2WANG_BARRETTS_ESOPHAGUS_DN
7	-19.8	NULL	55 / 572	Disease GUOJ_psooriasis_up
8	-19.24	NULL	7 / 19	BP peptide cross-linking
9	-16.94	NULL	1 / 6	GSEA C2SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
10	-16.46	NULL	4 / 15	MF retinol dehydrogenase activity
11	-16.3	NULL	16 / 76	BP epidermis development
12	-14.72	NULL	1 / 8	GSEA C2LIU_CDX2_TARGETS_DN
13	-13.9	NULL	5 / 15	GSEA C2HINATA_NFKB_TARGETS_KERATINOCYTE_DN
14	-12.36	NULL	1 / 10	GSEA C2MURAKAMI_UV_RESPONSE_1HR_UP
15	-11.74	NULL	5 / 16	GSEA C2ONDER_CDH1_TARGETS_3_DN
16	-11.67	NULL	1 / 11	GSEA C2MURAKAMI_UV_RESPONSE_6HR_DN
17	-11.43	NULL	1 / 6	GSEA C2GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN
18	-11.42	NULL	3 / 16	GSEA C2SMID_BREAST_CANCER_RELAPSE_IN_LUNG_UP
19	-11.27	NULL	4 / 44	CC keratin filament
20	-11.25	NULL	6 / 38	BP epithelial cell differentiation
21	-11.17	NULL	3 / 15	GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_E
22	-11.17	NULL	2 / 11	GSEA C2ROME_INSULIN_TARGETS_IN_MUSCLE_DN
23	-10.37	NULL	5 / 13	BP negative regulation of peptidase activity
24	-10.22	NULL	7 / 52	BP negative regulation of endopeptidase activity
25	-10.14	NULL	4 / 29	BP regulation of proteolysis
26	-9.89	NULL	10 / 122	MF serine-type endopeptidase activity
27	-9.69	NULL	1 / 9	GSEA C2NIKOLSKY_BREAST_CANCER_17P11_AMPLICON
28	-9.57	NULL	3 / 15	GSEA C2LEE_LIVER_CANCER_MYC_E2F1_UP
29	-9.47	NULL	3 / 18	BP retinol metabolic process
30	-9.43	NULL	3 / 16	GSEA C2CHEOK_RESPONSE_TO_MERCAPTOPYRINE_AND_LD_MTX_
31	-9.39	NULL	6 / 82	CC intermediate filament
32	-9.08	NULL	4 / 39	BP retinoid metabolic process
33	-8.87	NULL	1 / 9	GSEA C2REACTOME_ETHANOL_OXIDATION
34	-8.83	NULL	9 / 79	MF serine-type endopeptidase inhibitor activity
35	-8.78	NULL	12 / 186	MF structural molecule activity
36	-8.69	NULL	41 / 1182	CC extracellular region
37	-8.61	NULL	3 / 12	BP cellular aldehyde metabolic process
38	-8.6	NULL	6 / 16	GSEA C2SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
39	-8.37	NULL	2 / 15	GSEA C2PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
40	-8.17	NULL	1 / 12	GSEA C2ODDONNELL_METASTASIS_DN

